

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao

(ii) TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related Ligands and Uses Therefor

(iii) NUMBER OF SEQUENCES: 23

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Genentech, Inc.
- (B) STREET: 1 DNA Way
- (C) CITY: South San Francisco
- (D) STATE: California
- (E) COUNTRY: USA
- (F) ZIP: 94080

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: Unassigned
- (B) FILING DATE: 30-Jun-1998
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Conley, Deirdre L.
- (B) REGISTRATION NUMBER: 36,487
- (C) REFERENCE/DOCKET NUMBER: P1084R1-1

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 650/225-2066
- (B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2538 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: mouse NRG3 nucleic acid
- (B) LOCATION: 1-2538
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCTGACCGGC CGGCGGCGCC CGGGCCGGTC TCGCCCCTCT ACCGAGCGCC 50
TCGCCGCCCC CTCCCCGGCC CGCGTCCCCT CCCCCGTCCT CTCCTCCCCG 100
CCCGCCGCCC GCCTCTCGGG GGGAGGGGCG TGGGGGCAGG GAGCCGATTT 150
GCATGCGGCC GCCGCGGCCG CTGCCTGAGC CGGAGCCCGC CGCCGCCGGA 200
GCCCCGCGCC GCGCCCGCGC CCGGCCCGCG CGGCCCCATG CCTCTGGCGC 250
GGCCCTCGGG GGGGCGAAGG TGAAGATCGG CTCCTAGGAT GAGTGAAGGG 300
GCGGCCGGTG CCTCGCCACC TGGTGCCGCT TCGGCAGCCG CCGCCTCAGC 350
CGAGGAGGGC ACCGCGGCGG CTGCGGCGGC GGCGGCGGCG GGCGGGGGCC 400
CGGACGGCGG CGGAGAAGGG GCGGCCGAAC CCCCCGGGA GTTACGCTGT 450
AGCGACTGCA TCGTGTGGAA CCGGCAGCAG ACGTGGTTGT GCGTGGTGCC 500
TCTGTTCATC GGCTTCATCG GCCTGGGGCT CAGCCTCATG CTGCTTAAAT 550
GGATCGTGGT AGGCTCCGTC AAGGAGTACG TGCCCACGGA CCTGGTGGAC 600
TCCAAGGGAA TGGGCCAGGA CCCCTTCTTC CTCTCCAAGC CCAGCTCTTT 650
CCCCAAGGCT ATGGAAACCA CCACAACAAC CACTTCTACC ACGTCCCCCG 700
CCACCCCTC TGCCGGCGGC GCCGCTTCTT CCAGGACGCC TAACCGGATT 750
AGCACCCGCT TGACCACCAT CACACGGGCA CCCACCCGCT TCCCTGGGCA 800
CCGGGTTCCT ATCCGGGCTA GCCGCGCTC TACCACAGCA CGGAACACTG 850
CTGCCCCTCC GACGGTCCTG TCCACCACGG CCCCTTTCTT CAGTAGCAGC 900
ACGCCCCGGT CCCGACCCCC GATGCCAGGA GCCCCAGTA CGCAGGCGAT 950
GCCTTCCTGG CCCACTGCGG CGTATGCTAC CTCCTCCTAC CTCCACGATT 1000
CCACTCCCTC CTGGACCCTG TCACCCTTTC AGGATGCTGC TGCCGCCTCT 1050
TCCTCCTCAC CCTCTTCAC CTCCTCCACT ACCACCACCC CAGAACTAG 1100
CACCAGCCCC AAATTTTATA CTACAACATA CTCCACTGAA CGATCTGAGC 1150
ACTTCAAACC CTGTCGAGAC AAGGACCTGG CGTATTGTCT CAATGATGGT 1200

GAATGCTTTG TGATTGAGAC CCTGACAGGA TCCCATAAGC ACTGTCGGTG 1250
CAAGGAAGGC TACCAAGGAG TCCGTTGTGA TCAATTTCTG CCGAAAACAG 1300
ACTCCATCTT ATCGGATCCA ACAGACCACT TGGGGATTGA ATTCATGGAG 1350
AGTGAAGACG TTTATCAAAG GCAGGTGCTG TCAATTTTCAT GTATCATCTT 1400
TGGAATTGTC ATCGTGGGCA TGTTCGTGTC AGCATTCTAC TTCAAAAGCA 1450
AGAAACAAGC TAAACAAATT CAGGAGCACC TGAAAGAGTC ACAGAATGGG 1500
AAGAACTACA GCCTCAAGGC ATCCAGCACA AAGTCTGAGA GCTTGATGAA 1550
GAGCCATGTC CATCTACAAA ATTATTCAAA GGCGGATAGG CATCCTGTGA 1600
CTGCGCTGGA GAAAATAATG GAGTCAAGTT TTTCAGCTCC CCAGTCGTTT 1650
CCAGAAGTCA CTTCTCCTGA CCGAGGAAGC CAGCCTATCA AGCACCACAG 1700
CCCAGGACAA AGGAGTGGGA TGTTCATAG GAATACTTTC AGAAGGGCAC 1750
CACCCCTACC CCGAAGTCGA CTGGGTGGTA TTGTAGGACC AGCATATCAA 1800
CAACTTGAAG AATCAAGAAT TCCAGACCAG GATACGATAC CTTGCCAAGG 1850
GATAGAGGTC AGGAAGACTA TATCCCACCT GCCTATACAG CTGTGGTGTG 1900
TTGAAAGACC CCTGGACTTA AAGTATGTGT CCAATGGCTT AAGAACCCAA 1950
CAAATGCAT CAATAAATAT GCAACTGCCT TCAAGAGAGA CAAACCCCTA 2000
TTTTAATAGC TTGGATCAAA AGGACCTGGT GGGTTATTTA TCCCCAAGGG 2050
CCAATTCTGT GCCCATCATC CCGTCGATGG GTCTAGAAGA AACCTGCATG 2100
CAAATGCCAG GGATTTCTGA CGTCAAAAGC ATTAAATGGT GCAAAAACCTC 2150
CTACTCCGCT GACATTGTCA ACGCGAGTAT GCCAGTCAGT GATTGTCTTC 2200
TAGAAGAACA ACAGGAAGTG AAAATATTAC TAGAGACTGT GCAGGAACAG 2250
ATCCGGATTC TGACTGATGC CAGACGGTCA GAAGACTTCG AACTGGCCAG 2300
CATGGAACT GAGGACAGTG CGAGCGAAAA CACAGCCTTT CTCCCCCTGA 2350
GTCCCACGGC CAAATCAGAA CGAGAGGCAC AATTTGTCTT AAGAAATGAA 2400
ATACAAAGAG ACTCTGTGCT AACCAAGTGA CTGGAAATGT AGGAATCTGT 2450
GCATTATATG CTTTGCTAAA CAGGAAGGAG AGGAAATTAA ATACAAATTA 2500

TTTATATGCA TTAATTTAAG AGCATCTACT TAGAAGCC 2538

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Mouse NRG3 (mNRG3)/amino acid seq.
- (B) LOCATION: 1-713
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Glu	Gly	Ala	Ala	Gly	Ala	Ser	Pro	Pro	Gly	Ala	Ala	Ser	1	5	10	15
Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala	20	25	30	
Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala	35	40	45	
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp	50	55	60	
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	65	70	75	
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	80	85	90	
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser	95	100	105	
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser	110	115	120	
Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr	125	130	135	
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr	140	145	150	
Pro	Asn	Arg	Ile	Ser	Thr	Arg	Leu	Thr	Thr	Ile	Thr	Arg	Ala	Pro	155	160	165	
Thr	Arg	Phe	Pro	Gly	His	Arg	Val	Pro	Ile	Arg	Ala	Ser	Pro	Arg	170	175	180	

09877665-060801

Ser	Thr	Thr	Ala	Arg	Asn	Thr	Ala	Ala	Pro	Pro	Thr	Val	Leu	Ser	185	190	195
Thr	Thr	Ala	Pro	Phe	Phe	Ser	Ser	Ser	Thr	Pro	Gly	Ser	Arg	Pro	200	205	210
Pro	Met	Pro	Gly	Ala	Pro	Ser	Thr	Gln	Ala	Met	Pro	Ser	Trp	Pro	215	220	225
Thr	Ala	Ala	Tyr	Ala	Thr	Ser	Ser	Tyr	Leu	His	Asp	Ser	Thr	Pro	230	235	240
Ser	Trp	Thr	Leu	Ser	Pro	Phe	Gln	Asp	Ala	Ala	Ala	Ala	Ser	Ser	245	250	255
Ser	Ser	Pro	Ser	Ser	Thr	Ser	Ser	Thr	Thr	Thr	Thr	Pro	Glu	Thr	260	265	270
Ser	Thr	Ser	Pro	Lys	Phe	His	Thr	Thr	Thr	Tyr	Ser	Thr	Glu	Arg	275	280	285
Ser	Glu	His	Phe	Lys	Pro	Cys	Arg	Asp	Lys	Asp	Leu	Ala	Tyr	Cys	290	295	300
Leu	Asn	Asp	Gly	Glu	Cys	Phe	Val	Ile	Glu	Thr	Leu	Thr	Gly	Ser	305	310	315
His	Lys	His	Cys	Arg	Cys	Lys	Glu	Gly	Tyr	Gln	Gly	Val	Arg	Cys	320	325	330
Asp	Gln	Phe	Leu	Pro	Lys	Thr	Asp	Ser	Ile	Leu	Ser	Asp	Pro	Thr	335	340	345
Asp	His	Leu	Gly	Ile	Glu	Phe	Met	Glu	Ser	Glu	Asp	Val	Tyr	Gln	350	355	360
Arg	Gln	Val	Leu	Ser	Ile	Ser	Cys	Ile	Ile	Phe	Gly	Ile	Val	Ile	365	370	375
Val	Gly	Met	Phe	Cys	Ala	Ala	Phe	Tyr	Phe	Lys	Ser	Lys	Lys	Gln	380	385	390
Ala	Lys	Gln	Ile	Gln	Glu	His	Leu	Lys	Glu	Ser	Gln	Asn	Gly	Lys	395	400	405
Asn	Tyr	Ser	Leu	Lys	Ala	Ser	Ser	Thr	Lys	Ser	Glu	Ser	Leu	Met	410	415	420
Lys	Ser	His	Val	His	Leu	Gln	Asn	Tyr	Ser	Lys	Ala	Asp	Arg	His	425	430	435

Pro	Val	Thr	Ala	Leu 440	Glu	Lys	Ile	Met	Glu 445	Ser	Ser	Phe	Ser	Ala 450
Pro	Gln	Ser	Phe	Pro 455	Glu	Val	Thr	Ser	Pro 460	Asp	Arg	Gly	Ser	Gln 465
Pro	Ile	Lys	His	His 470	Ser	Pro	Gly	Gln	Arg 475	Ser	Gly	Met	Leu	His 480
Arg	Asn	Thr	Phe	Arg 485	Arg	Ala	Pro	Pro	Ser 490	Pro	Arg	Ser	Arg	Leu 495
Gly	Gly	Ile	Val	Gly 500	Pro	Ala	Tyr	Gln	Gln 505	Leu	Glu	Glu	Ser	Arg 510
Ile	Pro	Asp	Gln	Asp 515	Thr	Ile	Pro	Cys	Gln 520	Gly	Ile	Glu	Val	Arg 525
Lys	Thr	Ile	Ser	His 530	Leu	Pro	Ile	Gln	Leu 535	Trp	Cys	Val	Glu	Arg 540
Pro	Leu	Asp	Leu	Lys 545	Tyr	Val	Ser	Asn	Gly 550	Leu	Arg	Thr	Gln	Gln 555
Asn	Ala	Ser	Ile	Asn 560	Met	Gln	Leu	Pro	Ser 565	Arg	Glu	Thr	Asn	Pro 570
Tyr	Phe	Asn	Ser	Leu 575	Asp	Gln	Lys	Asp	Leu 580	Val	Gly	Tyr	Leu	Ser 585
Pro	Arg	Ala	Asn	Ser 590	Val	Pro	Ile	Ile	Pro 595	Ser	Met	Gly	Leu	Glu 600
Glu	Thr	Cys	Met	Gln 605	Met	Pro	Gly	Ile	Ser 610	Asp	Val	Lys	Ser	Ile 615
Lys	Trp	Cys	Lys	Asn 620	Ser	Tyr	Ser	Ala	Asp 625	Ile	Val	Asn	Ala	Ser 630
Met	Pro	Val	Ser	Asp 635	Cys	Leu	Leu	Glu	Glu 640	Gln	Gln	Glu	Val	Lys 645
Ile	Leu	Leu	Glu	Thr 650	Val	Gln	Glu	Gln	Ile 655	Arg	Ile	Leu	Thr	Asp 660
Ala	Arg	Arg	Ser	Glu 665	Asp	Phe	Glu	Leu	Ala 670	Ser	Met	Glu	Thr	Glu 675
Asp	Ser	Ala	Ser	Glu 680	Asn	Thr	Ala	Phe	Leu 685	Pro	Leu	Ser	Pro	Thr 690

	155		160		165
Thr Arg Phe Pro	Gly His Arg Val Pro	Ile Arg Ala Ser Pro	Arg		
	170	175	180		
Ser Thr Thr Ala	Arg Asn Thr Ala Ala	Pro Pro Thr Val Leu	Ser		
	185	190	195		
Thr Thr Ala Pro	Phe Phe Ser Ser Ser	Thr Pro Gly Ser Arg	Pro		
	200	205	210		
Pro Met Pro Gly	Ala Pro Ser Thr Gln	Ala Met Pro Ser Trp	Pro		
	215	220	225		
Thr Ala Ala Tyr	Ala Thr Ser Ser Tyr	Leu His Asp Ser Thr	Pro		
	230	235	240		
Ser Trp Thr Leu	Ser Pro Phe Gln Asp	Ala Ala Ala Ala Ser	Ser		
	245	250	255		
Ser Ser Pro Ser	Ser Thr Ser Ser Thr	Thr Thr Thr Pro Glu	Thr		
	260	265	270		
Ser Thr Ser Pro	Lys Phe His Thr Thr	Thr Tyr Ser Thr Glu	Arg		
	275	280	285		
Ser Glu His Phe	Lys Pro Cys Arg Asp	Lys Asp Leu Ala Tyr	Cys		
	290	295	300		
Leu Asn Asp Gly	Glu Cys Phe Val Ile	Glu Thr Leu Thr Gly	Ser		
	305	310	315		
His Lys His Cys	Arg Cys Lys Glu Gly	Tyr Gln Gly Val Arg	Cys		
	320	325	330		
Asp Gln Phe Leu	Pro Lys Thr Asp Ser	Ile Leu Ser Asp Pro	Thr		
	335	340	345		
Asp His Leu Gly	Ile Glu Phe Met Glu	Ser Glu Asp Val Tyr	Gln		
	350	355	360		
Arg Gln					
	362				

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 47 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

(2) INFORMATION FOR SEQ ID NO:5:

(ix) FEATURE:

(A) NAME/KEY: Human NRG3B1(hNRG3B1)/nucleic acid seq.
(B) LOCATION: 1-2502
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

102

CAAATGGATC GTGGTGGGCT CCGTCAAGGA GTACGTGCCC ACCGACCTAG 450
TGGACTCCAA GGGGATGGGC CAGGACCCCT TCTTCCTCTC CAAGCCCAGC 500
TCTTTCCCCA AGGCCATGGA GACCACCACC ACTACCACTT CCACCACGTC 550
CCCCGCCACC CCCTCCGCCG GGGGTGCCGC CTCCTCCAGG ACGCCCAACC 600
GGATTAGCAC TCGCCTGACC ACCATCACGC GGGCGCCCAC TCGCTTCCCC 650
GGGCACCGGG TGCCCATCCG GGCCAGCCCG CGCTCCACCA CAGCACGGAA 700
CACTGCGGCC CCTGCGACGG TCCCGTCCAC CACGGCCCCG TTCTTCAGTA 750
GCAGCACGCT GGGCTCCCGA CCCCCGGTGC CAGGAACTCC AAGTACCCAG 800
GCAATGCCCT CCTGGCCTAC TGCGGCATA C GCTACCTCCT CCTACCTTCA 850
CGATTCTACT CCCTCCTGGA CCCTGTCTCC CTTTCAGGAT GCTGCCTCCT 900
CTTCTTCCTC TTCTTCCTCC TCCGCTACCA CCACCACACC AGAAACTAGC 950
ACCAGCCCCA AATTCATAC GACGACATAT TCCACAGAGC GATCCGAGCA 1000
CTTCAAACCC TGCCGAGACA AGGACCTTGC ATACTGTCTC AATGATGGCG 1050
AGTGCTTTGT GATCGAAACC CTGACCGGAT CCCATAAACA CTGTCGGTGC 1100
AAAGAAGGCT ACCAAGGAGT CCGTTGTGAT CAATTTCTGC CGAAAACCTGA 1150
TTCCATCTTA TCGGATCCAA CAGACCACTT GGGGATTGAA TTCATGGAGA 1200
GTGAAGAAGT TTATCAAAGG CAGGTGCTGT CAATTTCATG TATCATCTTT 1250
GGAATTGTCA TCGTGGGCAT GTTCTGTGCA GCATTCTACT TCAAAAGCAA 1300
GAAACAAGCT AAACAAATCC AAGAGCAGCT GAAAGTGCCA CAAAATGGTA 1350
AAAGCTACAG TCTCAAAGCA TCCAGCACAA TGGCAAAGTC AGAGAACTTG 1400
GTGAAGAGCC ATGTCCAGCT GCAAAATTAT TCAAAGGTGG AAAGGCATCC 1450
TGTGACTGCA TTGGAGAAAA TGATGGAGTC AAGTTTTGTC GGCCCCCAGT 1500
CATTCCCTGA GGTCCCTTCT CCTGACAGAG GAAGCCAGTC TGTCAAACAC 1550
CACAGGAGTC TATCCTCTTG CTGCAGCCCA GGGCAAAGAA GTGGCATGCT 1600
CCATAGGAAT GCCTTCAGAA GGACACCCCC GTCACCCCGA AGTAGGCTAG 1650
GTGGAATTGT GGGACCAGCA TATCAGCAAC TCGAAGAATC AAGGATCCCA 1700

GACCAGGATA CGATACCTTG CCAAGGGATA GAGGTCAGGA AGACTATATC 1750
 CCACCTGCCT ATACAGCTGT GGTGTGTTGA AAGACCCCTG GACTTAAAGT 1800
 ATTCATCCAG TGGTTTAAAA ACCCAACGAA ATACATCAAT AAATATGCAA 1850
 CTGCCTTCAA GAGAGACAAA CCCCTATTTT AATAGCTTGG AGCAAAAGGA 1900
 CCTGGTGGGC TATTCATCCA CAAGGGCCAG TTCTGTGCCC ATCATCCCTT 1950
 CAGTGGGTTT AGAGGAAACC TGCCTGCAAA TGCCAGGGAT TTCTGAAGTC 2000
 AAAAGCATCA AATGGTGCAA AAACCTCTAT TCAGCTGACG TTGTCAATGT 2050
 GAGTATTCCA GTCAGCGATT GTCTTATAGC AGAACAACAA GAAGTGAAAA 2100
 TATTGCTAGA AACTGTCCAG GAGCAGATCC GAATTCTGAC TGATGCCAGA 2150
 CGGTCAGAAG ACTACGAACT GGCCAGCGTA GAAACCGAGG ACAGTGCAAG 2200
 CGAAAACACA GCCTTTCTCC CCCTGAGTCC CACAGCCAAA TCAGAACGAG 2250
 AGGCGCAATT TGTCTTAAGA AATGAAATAC AAAGAGACTC TGCATTGACC 2300
 AAGTGACTION AGATGTAGGA ATCTGTGCAT TCTATGCTTT GCTCAACAGG 2350
 AAAGAGAGGA AATCAAATAC AAATTATTTA TATGCATTAA TTTAAGAGCA 2400
 TCTACTTAGA AGAAACCAAA TAGTCTATCG CCCTCATATC ATAGTGTTTT 2450
 TTAACAAAAT ATTTTTTTTAA GGGAAAGAAA TGTTTCAGGA GGGATAAAGC 2500
 TT 2502

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hNRG3B1 amino acid sequence
- (B) LOCATION: 1-720
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ser	Glu	Gly	Ala	Ala	Ala	Ala	Ser	Pro	Pro	Gly	Ala	Ala	Ser
1				5					10					15

Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala	20	25	30
Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala	35	40	45
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp	50	55	60
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	65	70	75
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	80	85	90
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser	95	100	105
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser	110	115	120
Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr	125	130	135
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr	140	145	150
Pro	Asn	Arg	Ile	Ser	Thr	Arg	Leu	Thr	Thr	Ile	Thr	Arg	Ala	Pro	155	160	165
Thr	Arg	Phe	Pro	Gly	His	Arg	Val	Pro	Ile	Arg	Ala	Ser	Pro	Arg	170	175	180
Ser	Thr	Thr	Ala	Arg	Asn	Thr	Ala	Ala	Pro	Ala	Thr	Val	Pro	Ser	185	190	195
Thr	Thr	Ala	Pro	Phe	Phe	Ser	Ser	Ser	Thr	Leu	Gly	Ser	Arg	Pro	200	205	210
Pro	Val	Pro	Gly	Thr	Pro	Ser	Thr	Gln	Ala	Met	Pro	Ser	Trp	Pro	215	220	225
Thr	Ala	Ala	Tyr	Ala	Thr	Ser	Ser	Tyr	Leu	His	Asp	Ser	Thr	Pro	230	235	240
Ser	Trp	Thr	Leu	Ser	Pro	Phe	Gln	Asp	Ala	Ala	Ser	Ser	Ser	Ser	245	250	255
Ser	Ser	Ser	Ser	Ser	Ala	Thr	Thr	Thr	Thr	Pro	Glu	Thr	Ser	Thr	260	265	270

Ser	Pro	Lys	Phe	His	Thr	Thr	Thr	Tyr	Ser	Thr	Glu	Arg	Ser	Glu	275	280	285
His	Phe	Lys	Pro	Cys	Arg	Asp	Lys	Asp	Leu	Ala	Tyr	Cys	Leu	Asn	290	295	300
Asp	Gly	Glu	Cys	Phe	Val	Ile	Glu	Thr	Leu	Thr	Gly	Ser	His	Lys	305	310	315
His	Cys	Arg	Cys	Lys	Glu	Gly	Tyr	Gln	Gly	Val	Arg	Cys	Asp	Gln	320	325	330
Phe	Leu	Pro	Lys	Thr	Asp	Ser	Ile	Leu	Ser	Asp	Pro	Thr	Asp	His	335	340	345
Leu	Gly	Ile	Glu	Phe	Met	Glu	Ser	Glu	Glu	Val	Tyr	Gln	Arg	Gln	350	355	360
Val	Leu	Ser	Ile	Ser	Cys	Ile	Ile	Phe	Gly	Ile	Val	Ile	Val	Gly	365	370	375
Met	Phe	Cys	Ala	Ala	Phe	Tyr	Phe	Lys	Ser	Lys	Lys	Gln	Ala	Lys	380	385	390
Gln	Ile	Gln	Glu	Gln	Leu	Lys	Val	Pro	Gln	Asn	Gly	Lys	Ser	Tyr	395	400	405
Ser	Leu	Lys	Ala	Ser	Ser	Thr	Met	Ala	Lys	Ser	Glu	Asn	Leu	Val	410	415	420
Lys	Ser	His	Val	Gln	Leu	Gln	Asn	Tyr	Ser	Lys	Val	Glu	Arg	His	425	430	435
Pro	Val	Thr	Ala	Leu	Glu	Lys	Met	Met	Glu	Ser	Ser	Phe	Val	Gly	440	445	450
Pro	Gln	Ser	Phe	Pro	Glu	Val	Pro	Ser	Pro	Asp	Arg	Gly	Ser	Gln	455	460	465
Ser	Val	Lys	His	His	Arg	Ser	Leu	Ser	Ser	Cys	Cys	Ser	Pro	Gly	470	475	480
Gln	Arg	Ser	Gly	Met	Leu	His	Arg	Asn	Ala	Phe	Arg	Arg	Thr	Pro	485	490	495
Pro	Ser	Pro	Arg	Ser	Arg	Leu	Gly	Gly	Ile	Val	Gly	Pro	Ala	Tyr	500	505	510
Gln	Gln	Leu	Glu	Glu	Ser	Arg	Ile	Pro	Asp	Gln	Asp	Thr	Ile	Pro	515	520	525

Cys	Gln	Gly	Ile	Glu	Val	Arg	Lys	Thr	Ile	Ser	His	Leu	Pro	Ile	530	535	540
Gln	Leu	Trp	Cys	Val	Glu	Arg	Pro	Leu	Asp	Leu	Lys	Tyr	Ser	Ser	545	550	555
Ser	Gly	Leu	Lys	Thr	Gln	Arg	Asn	Thr	Ser	Ile	Asn	Met	Gln	Leu	560	565	570
Pro	Ser	Arg	Glu	Thr	Asn	Pro	Tyr	Phe	Asn	Ser	Leu	Glu	Gln	Lys	575	580	585
Asp	Leu	Val	Gly	Tyr	Ser	Ser	Thr	Arg	Ala	Ser	Ser	Val	Pro	Ile	590	595	600
Ile	Pro	Ser	Val	Gly	Leu	Glu	Glu	Thr	Cys	Leu	Gln	Met	Pro	Gly	605	610	615
Ile	Ser	Glu	Val	Lys	Ser	Ile	Lys	Trp	Cys	Lys	Asn	Ser	Tyr	Ser	620	625	630
Ala	Asp	Val	Val	Asn	Val	Ser	Ile	Pro	Val	Ser	Asp	Cys	Leu	Ile	635	640	645
Ala	Glu	Gln	Gln	Glu	Val	Lys	Ile	Leu	Leu	Glu	Thr	Val	Gln	Glu	650	655	660
Gln	Ile	Arg	Ile	Leu	Thr	Asp	Ala	Arg	Arg	Ser	Glu	Asp	Tyr	Glu	665	670	675
Leu	Ala	Ser	Val	Glu	Thr	Glu	Asp	Ser	Ala	Ser	Glu	Asn	Thr	Ala	680	685	690
Phe	Leu	Pro	Leu	Ser	Pro	Thr	Ala	Lys	Ser	Glu	Arg	Glu	Ala	Gln	695	700	705
Phe	Val	Leu	Arg	Asn	Glu	Ile	Gln	Arg	Asp	Ser	Ala	Leu	Thr	Lys	710	715	720

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hNRG3 extracellular domain/Amino AcidSeq
- (B) LOCATION: 1-360
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Ser	Glu	Gly	Ala	Ala	Ala	Ala	Ser	Pro	Pro	Gly	Ala	Ala	Ser	1	5	10	15
Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala	20	25	30	
Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala	35	40	45	
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp	50	55	60	
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	65	70	75	
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	80	85	90	
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser	95	100	105	
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser	110	115	120	
Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr	125	130	135	
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr	140	145	150	
Pro	Asn	Arg	Ile	Ser	Thr	Arg	Leu	Thr	Thr	Ile	Thr	Arg	Ala	Pro	155	160	165	
Thr	Arg	Phe	Pro	Gly	His	Arg	Val	Pro	Ile	Arg	Ala	Ser	Pro	Arg	170	175	180	
Ser	Thr	Thr	Ala	Arg	Asn	Thr	Ala	Ala	Pro	Ala	Thr	Val	Pro	Ser	185	190	195	
Thr	Thr	Ala	Pro	Phe	Phe	Ser	Ser	Ser	Thr	Leu	Gly	Ser	Arg	Pro	200	205	210	
Pro	Val	Pro	Gly	Thr	Pro	Ser	Thr	Gln	Ala	Met	Pro	Ser	Trp	Pro	215	220	225	
Thr	Ala	Ala	Tyr	Ala	Thr	Ser	Ser	Tyr	Leu	His	Asp	Ser	Thr	Pro	230	235	240	
Ser	Trp	Thr	Leu	Ser	Pro	Phe	Gln	Asp	Ala	Ala	Ser	Ser	Ser	Ser	245	250	255	

Ser	Ser	Ser	Ser	Ser	Ala	Thr	Thr	Thr	Thr	Pro	Glu	Thr	Ser	Thr
				260						265				270
Ser	Pro	Lys	Phe	His	Thr	Thr	Thr	Tyr	Ser	Thr	Glu	Arg	Ser	Glu
				275					280					285
His	Phe	Lys	Pro	Cys	Arg	Asp	Lys	Asp	Leu	Ala	Tyr	Cys	Leu	Asn
				290					295					300
Asp	Gly	Glu	Cys	Phe	Val	Ile	Glu	Thr	Leu	Thr	Gly	Ser	His	Lys
				305					310					315
His	Cys	Arg	Cys	Lys	Glu	Gly	Tyr	Gln	Gly	Val	Arg	Cys	Asp	Gln
				320					325					330
Phe	Leu	Pro	Lys	Thr	Asp	Ser	Ile	Leu	Ser	Asp	Pro	Thr	Asp	His
				335					340					345
Leu	Gly	Ile	Glu	Phe	Met	Glu	Ser	Glu	Glu	Val	Tyr	Gln	Arg	Gln
				350					355					360

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: NRG3 EGF-like domain/amino acid seq.
- (B) LOCATION: 1-47
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

His	Phe	Lys	Pro	Cys	Arg	Asp	Lys	Asp	Leu	Ala	Tyr	Cys	Leu	Asn
1				5					10					15
Asp	Gly	Glu	Cys	Phe	Val	Ile	Glu	Thr	Leu	Thr	Gly	Ser	His	Lys
				20					25					30
His	Cys	Arg	Cys	Lys	Glu	Gly	Tyr	Gln	Gly	Val	Arg	Cys	Asp	Gln
				35					40					45
Phe	Leu													
	47													

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(A) LENGTH: 48 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(A) NAME/KEY: cARIA.egf
(B) LOCATION: 1-48
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

[illegible]

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(A) NAME/KEY: hAR.egf
(B) LOCATION: 1-45
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

Lys Lys Asn Pro Cys Asn Ala Glu Phe Gln Asn Phe Cys Ile His
1 5 10 15

Gly Glu Cys Lys Tyr Ile Glu His Leu Glu Ala Val Thr Cys Lys
20 25 30

Cys Gln Gln Glu Tyr Phe Gly Glu Arg Cys Gly Glu Lys Ser Met
35 40 45

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hBTC.efg
(B) LOCATION: 1-45
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

His Phe Ser Arg Cys Pro Lys Gln Tyr Lys His Tyr Cys Ile Lys
1 5 10 15
Gly Arg Cys Arg Phe Val Val Ala Glu Gln Thr Pro Ser Cys Val
20 25 30
Cys Asp Glu Gly Tyr Ile Gly Ala Arg Cys Glu Arg Val Asp Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hEGF.egf
(B) LOCATION: 1-46
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His
1 5 10 15
Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys
20 25 30
Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp
35 40 45
Leu
46

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

- (ix) FEATURE:
(A) NAME/KEY: hHB-EGF.egf
(B) LOCATION: 1-45
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys Ile His
1 5 10 15
Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys Ile
20 25 30
Cys His Pro Gly Tyr His Gly Glu Arg Cys His Gly Leu Ser Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

- (ix) FEATURE:
(A) NAME/KEY: hHRGalpha.egf
(B) LOCATION: 1-49
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1 5 10 15
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg
20 25 30
Tyr Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr
35 40 45
Glu Asn Tyr Pro
49

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hHRGbeta.egf
(B) LOCATION: 1-48
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1 5 10 15
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg
20 25 30
Tyr Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln
35 40 45
Asn Tyr Val
48

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hTGFalpha.egf
(B) LOCATION: 1-45
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

His Phe Asn Asp Cys Pro Asp Ser His Thr Gln Phe Cys Phe His
1 5 10 15
Gly Thr Cys Arg Phe Leu Val Gln Glu Asp Lys Pro Ala Cys Val
20 25 30
Cys His Ser Gly Tyr Val Gly Ala Arg Cys Glu His Ala Asp Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: mEPR.egf
(B) LOCATION: 1-45
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gln Ile Thr Lys Cys Ser Ser Asp Met Asp Gly Tyr Cys Leu His
1 5 10 15
Gly Gln Cys Ile Tyr Leu Val Asp Met Arg Glu Lys Phe Cys Arg
20 25 30
Cys Glu Val Gly Tyr Thr Gly Leu Arg Cys Glu His Phe Phe Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Oligonucleotide probe
(B) LOCATION: 1-50
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Thr Gly Gly Thr Ala Ala Ala Ala Gly Cys Thr Ala Cys Ala Gly
1 5 10 15
Thr Cys Thr Cys Ala Ala Ala Gly Cys Ala Thr Cys Cys Ala Gly
20 25 30
Cys Ala Cys Ala Ala Thr Gly Gly Cys Ala Ala Ala Gly Thr Cys
35 40 45
Ala Gly Ala Gly Ala
50

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(A) LENGTH: 8 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(A) NAME/KEY: hNRG3B1 transmembrane proximal 1
(B) LOCATION: 1-8
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

Asn Asp Gly Glu Cys Phe Val Ile
1 5 8

(A) LENGTH: 9 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(A) NAME/KEY: hNRG3B1 transmembrane proximal 2
(B) LOCATION: 1-9
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

Glu Phe Met Glu Ser Glu Glu Val Tyr
1 5 9

(A) LENGTH: 466 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(A) NAME/KEY: EST Genbank entry H23651
(B) LOCATION: 1-466
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AATTTCTGCC GAAAACTGAT TCCATCTTAT CGGATCCAAC AGACCACTTG 50
GGGATTGAAT TCATGGAGAG TGAAGAAGTT TATCAAAGGC AGGTGCTGTC 100
AATTTTCATGT ATCATCTTTG GAATTGTCAT CGTGGGCATG TTCTGTGCAG 150
CATTCTACTT CAAAAGCAAG AAACAAGCTA AACAAATCCA AGAGCAGCTG 200
AAAGTGCCAC AAAATGGTAA AAGCTACAGT CTCAAAGCAT CCAGCACAAT 250
GGCAAAGTCA GAGAACTTGG TGAAGAGCCA TGTCCAGCTG CAAAATAAAA 300
TGTCAGGCTT CTGAGCCCAA GCTAAGCCAT CATATCCCCT GTNGACCTGC 350
ACGTGCACAT CCNGATGGCC CGTTTCCTGC CTTTNTGAT GACATTTNCA 400
CCACAAATGN AGTGAAAATG GGNCTTTTCN TGCCTTAACT GGTGACNTT 450
TTNCCCCAA AAGGAG 466

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2091 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATGAGTGAAG GGGCGGCCGC TGCCTCGCCA CCTGGTGCCG CTCGGCAGC 50
CGCCGCCTCG GCCGAGGAGG GCACCGCGGC GGCTGCGGCG GCGGCAGCGG 100
CGGGCGGGGG CCCGGACGGC GGCGGCGAAG GGGCGGCCGA GCCCCC CGG 150
GAGTTACGCT GTAGCGACTG CATCGTGTGG AACCGGCAGC AGACGTGGCT 200
GTGCGTGGTA CCTCTGTTCA TCGGCTTCAT CGGCCTGGGG CTCAGCCTCA 250
TGCTTCTCAA ATGGATCGTG GTGGGCTCCG TCAAGGAGTA CGTGCCCACC 300
GACCTAGTGG ACTCCAAGGG GATGGGCCAG GACCCCTTCT TCCTCTCCAA 350
GCCCAGCTCT TTCCCCAAGG CCATGGAGAC CACCACCACT ACCACTTCCA 400
CCACGTCCCC CGCCACCCCC TCCGCCGGGG GTGCCGCCTC CTCCAGGACG 450

CCCAACCGGA TTAGCACTCG CCTGACCACC ATCACGCGGG CGCCCACTCG 500
 CTTCCCCGGG CACCGGGTGC CCATCCGGGC CAGCCCGCGC TCCACCACAG 550
 CACGGAACAC TGCGGCCCCT GCGACGGTCC CGTCCACCAC GGCCCCGTTC 600
 TTCAGTAGCA GCACGCTGGG CTCCCGACCC CCGGTGCCAG GAACTCCAAG 650
 TACCCAGGCA ATGCCCTCCT GGCCTACTGC GGCATACGCT ACCTCCTCCT 700
 ACCTTCACGA TTCTACTCCC TCCTGGACCC TGTCTCCCTT TCAGGATGCT 750
 GCCTCCTCTT CTTCTCTTC TTCCTCCTCC GCTACCACCA CCACACCAGA 800
 AACTAGCACC AGCCCCAAT TTCATACGAC GACATATTCC ACAGAGCGAT 850
 CCGAGCACTT CAAACCCTGC CGAGACAAGG ACCTTGCATA CTGTCTCAAT 900
 GATGGCGAGT GCTTTGTGAT CGAAACCCTG ACCGGATCCC ATAAACACTG 950
 TCGGTGCAA GAAGGCTACC AAGGAGTCCG TTGTGATCAA TTTCTGCCGA 1000
 AAAGTATTC CATCTTATCG GATCCAACAG ACCACTTGGG GATTGAATTC 1050
 ATGGAGAGTG AAGAAGTTTA TCAAAGGCAG GTGCTGTCAA TTTCATGTAT 1100
 CATCTTTGGA ATTGTCATCG TGGGCATGTT CTGTGCAGCA TTCTACTTCA 1150
 AAAGCAAGAA ACAAGCTAAA CAAATCCAAG AGCAGCTGAA AGTGCCACAA 1200
 AATGGTAAAA GCTACAGTCT CAAAGCATCC AGCACAATGG CAAAGTCAGA 1250
 GAACTTGGTG AAGAGCCATG TCCAGCTGCA AAATTATTCA AAGGTGGAAA 1300
 GGCATCCTGT GACTGCATTG GAGAAAATGA TGGAGTCAAG TTTTGTCTGC 1350
 CCCCAGTCAT TCCCTGAGGT CCCTTCTCCT GACAGAGGAA GCCAGTCTGT 1400
 CAAACACCAC AGGAGTCTAT CCTCTTGCTG CAGCCCAGGG CAAAGAAGTG 1450
 GCATGCTCCA TAGGAATGCC TTCAGAAGGA CACCCCCGTC ACCCCGAAGT 1500
 AGGCTAGGTG GAATTGTGGG ACCAGCATAT CAGCAACTCG AAGAATCAAG 1550
 GATCCCAGAC CAGGATACGA TACCTTGCCA AGGGTATTCA TCCAGTGGTT 1600
 TAAAAACCCA ACGAAATACA TCAATAAATA TGCAACTGCC TTCAAGAGAG 1650
 ACAAACCCCT ATTTTAATAG CTTGGAGCAA AAGGACCTGG TGGGCTATTC 1700
 ATCCACAAGG GCCAGTTCTG TGCCCATCAT CCCTTCAGTG GGTTTAGAGG 1750

AACCTGCCT GCAAATGCCA GGGATTTCTG AAGTCAAAAG CATCAAATGG 1800
 TGCAAAAACCT CCTATTCAGC TGACGTTGTC AATGTGAGTA TTCCAGTCAG 1850
 CGATTGTCTT ATAGCAGAAC AACAAGAAGT GAAAATATTG CTAGAAACTG 1900
 TCCAGGAGCA GATCCGAATT CTGACTGATG CCAGACGGTC AGAAGACTAC 1950
 GAACTGGCCA GCGTAGAAAC CGAGGACAGT GCAAGCGAAA ACACAGCCTT 2000
 TCTCCCCCTG AGTCCCACAG CCAAATCAGA ACGAGAGGCG CAATTTGTCT 2050
 TAAGAAATGA AATACAAAGA GACTCTGCAT TGACCAAGTG A 2091

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 696 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Human NRG3B2
- (B) LOCATION: 1-696
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Ser	Glu	Gly	Ala	Ala	Ala	Ala	Ser	Pro	Pro	Gly	Ala	Ala	Ser	1	5	10	15
Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala	20	25	30	
Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala	35	40	45	
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp	50	55	60	
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	65	70	75	
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	80	85	90	
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser	95	100	105	
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser	110	115	120	

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Met	Phe	Cys	Ala	Ala	Phe	Tyr	Phe	Lys	Ser	Lys	Lys	Gln	Ala	Lys	
				380					385					390	
Gln	Ile	Gln	Glu	Gln	Leu	Lys	Val	Pro	Gln	Asn	Gly	Lys	Ser	Tyr	
				395					400					405	
Ser	Leu	Lys	Ala	Ser	Ser	Thr	Met	Ala	Lys	Ser	Glu	Asn	Leu	Val	
				410					415					420	
Lys	Ser	His	Val	Gln	Leu	Gln	Asn	Tyr	Ser	Lys	Val	Glu	Arg	His	
				425					430					435	
Pro	Val	Thr	Ala	Leu	Glu	Lys	Met	Met	Glu	Ser	Ser	Phe	Val	Gly	
				440					445					450	
Pro	Gln	Ser	Phe	Pro	Glu	Val	Pro	Ser	Pro	Asp	Arg	Gly	Ser	Gln	
				455					460					465	
Ser	Val	Lys	His	His	Arg	Ser	Leu	Ser	Ser	Cys	Cys	Ser	Pro	Gly	
				470					475					480	
Gln	Arg	Ser	Gly	Met	Leu	His	Arg	Asn	Ala	Phe	Arg	Arg	Thr	Pro	
				485					490					495	
Pro	Ser	Pro	Arg	Ser	Arg	Leu	Gly	Gly	Ile	Val	Gly	Pro	Ala	Tyr	
				500					505					510	
Gln	Gln	Leu	Glu	Glu	Ser	Arg	Ile	Pro	Asp	Gln	Asp	Thr	Ile	Pro	
				515					520					525	
Cys	Gln	Gly	Tyr	Ser	Ser	Ser	Gly	Leu	Lys	Thr	Gln	Arg	Asn	Thr	
				530					535					540	
Ser	Ile	Asn	Met	Gln	Leu	Pro	Ser	Arg	Glu	Thr	Asn	Pro	Tyr	Phe	
				545					550					555	
Asn	Ser	Leu	Glu	Gln	Lys	Asp	Leu	Val	Gly	Tyr	Ser	Ser	Thr	Arg	
				560					565					570	
Ala	Ser	Ser	Val	Pro	Ile	Ile	Pro	Ser	Val	Gly	Leu	Glu	Glu	Thr	
				575					580					585	
Cys	Leu	Gln	Met	Pro	Gly	Ile	Ser	Glu	Val	Lys	Ser	Ile	Lys	Trp	
				590					595					600	
Cys	Lys	Asn	Ser	Tyr	Ser	Ala	Asp	Val	Val	Asn	Val	Ser	Ile	Pro	
				605					610					615	
Val	Ser	Asp	Cys	Leu	Ile	Ala	Glu	Gln	Gln	Glu	Val	Lys	Ile	Leu	
				620					625					630	

